

AAZ36836
ID: AAZ36836 standard; cDNA; 1067 BP.

AAZ36836;

13-MAR-2000 (first entry)

Nucleotide sequence of human Interleukin-21.

Human; Interleukin-22; IL-22; IL-21; Immune system disorder;

Immune cell chemotaxis; haematopoietic cell disorder;

haemostatic activity; thrombolytic activity; autoimmune disorder; asthma;

respiratory problem; organ rejection; graft-versus-host disease; GVHD;

Inflammation; hyperproliferative disorder; tissue regeneration;

embryonic stem cell differentiation; embryonic stem cell proliferation;

haematopoietic lineage; allergic asthma; ss.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 34..627

FT /tag= a

FT /product= "IL-21"

FT sig_peptide 34..1060

FT /tag= b

FT sig_peptide 34..87

FT /tag= c

MO9961617-A1.

02-DEC-1999.

27-MAY-1999; 99WO-US11644.

29-MAY-1998; 98US-0087340.

10-SEP-1998; 98US-0099805.

30-APR-1999; 99US-0131965.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Ebner R;

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The present sequence encodes a human Interleukin-21 (IL-21) protein. The specification also describes IL-22 polynucleotides and polypeptides. The IL-21 polynucleotide was isolated from a cDNA library of apoptotic T-cells. IL-21 and IL-22 may be useful in treating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells, treating or detecting deficiencies of haematopoietic cells, to modulate haemostatic or thrombolytic activity, in treating or detecting autoimmune disorders, treating asthma (particularly allergic asthma) or other respiratory problems, to treat-and/or prevent organ rejection or graft-versus-host disease (GVHD), to modulate inflammation, to treat or detect hyperproliferative disorders, to treat or detect infectious agents, to differentiate, proliferate and attract cells, leading to the regeneration of tissues, IL-21 and IL-22 may also increase or decrease the differentiation or proliferation of embryonic stem cells and haematopoietic lineage, may be used to modulate mammalian characteristics.

Sequence 1067 BP; 215 A; 371 C; 273 G; 206 T; 2 other;

Match 96.1%; Score 1006.4; DB 21; Length 1067;

Best Local Similarity 98.9%; Pred. No. 4,4e-231; Matches 1021; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY	17	gtctcaagccagcctgcccgcgtgcgcgcacacatgacgctcctccgcgctctgttt	76
DB	1	gtctcaagccagcctgcccgcgtgcgcgcacacatgacgctcctccgcgctctgttt	60
QY	77	ctgacccgtgctgacacatgctgctgcccacatgacccctccctcagggggacccac	136
DB	61	ctgacccgtgctgacacatgctgctgcccacatgacccctccctcagggggacccac	120
QY	137	agtaacggtacccacacatgctgctgctgaggaactgcccctcggcaggcccccca	196
DB	121	agtaacggtacccacacatgctgctgctgaggaactgcccctcggcaggcccccca	180
QY	197	cactgctgctgctgaggtgacagtgaggcaggcttgcctgtagcctgtgtccagc	256
DB	181	cactgctgctgctgaggtgacagtgaggcaggcttgcctgtagcctgtgtccagc	240
QY	257	ctgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	316
DB	241	ctgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	300
QY	317	gtgctgctgctgagagaggtgttgaggcagacacccacagcgtctcatctcaccctg	376
DB	301	gtgctgctgctgagagaggtgttgaggcagacacccacagcgtctcatctcaccctg	360
QY	377	agataccgtgtggaacagcagatgagagcagcagcagcagcagcagcagcagcagc	436
DB	361	agataccgtgtggaacagcagatgagagcagcagcagcagcagcagcagcagcagc	420
QY	437	ctgtgacagagctgcatcagatgacagcagcagcagcagcagcagcagcagcagc	496
DB	421	ctgtgacagagctgcatcagatgacagcagcagcagcagcagcagcagcagcagc	480
QY	497	cggctgctcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	556
DB	481	cggctgctcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	540
QY	557	ctcccccacacccctgggcttgccttccacacagcagcagcagcagcagcagcagc	616
DB	541	ctcccccacacccctgggcttgccttccacacagcagcagcagcagcagcagcagc	600
QY	617	acctgctgctgcccgccttgccttccacacagcagcagcagcagcagcagcagcagc	676
DB	601	acctgctgctgcccgccttgccttccacacagcagcagcagcagcagcagcagcagc	660
QY	677	gtgtgctcccaagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	736
DB	661	gtgtgctcccaagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	720
QY	737	ccaacacacacccctgggcttgccttccacacagcagcagcagcagcagcagcagc	796
DB	721	ccaacacacacccctgggcttgccttccacacagcagcagcagcagcagcagcagc	780
QY	797	tctcaatcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	856
DB	781	tctcaatcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	840
QY	857	aaagctgcaaaaaggtgtacacagcagcagcagcagcagcagcagcagcagcagc	916
DB	841	aaagctgcaaaaaggtgtacacagcagcagcagcagcagcagcagcagcagcagc	900
QY	917	cttccttaccatactgctcagg-ccccgagagcagcagcagcagcagcagcagcagc	975
DB	901	cttccttaccatactgctcagg-ccccgagagcagcagcagcagcagcagcagcagc	960
QY	976	gaagtaacctgtttcttaacaattatgaagtgatgataattataaactgagac	1035
DB	961	gaagtaacctgtttcttaacaattatgaagtgatgataattataaactgagac	1020
QY	1036	acatcccccaaa 1047	

Query Match 100.0%; Score 1073; DB 21; Length 197;
 Best Local Similarity 100.0%; Pred. No. 4.6e-109;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLFLTWLHTCLAHNDPSLRGPHSHGTPHCYSAEELPLGOAPPHLLARGAKWQ 60
 DB 1 mtlplglfltlwlnhtclahndpslrghshgtpchysaeelpigqaphllargakwq 60
 QY 61 ALPALVSSLEAASHRGHERPSATTOCPVLRPEEVLEADTHQHSISPMRYRVDTDEDRY 120
 DB 61 alpavlsleaashrgherpsattpcvlrpeeveleadthqrsispwryrvdtdedry 120
 QY 121 POKLAFAECCLRGCDARTGRETALNSVRLQSLVLRPRCSRDGSLPTPGAFAPFT 180
 DB 121 pklafaeclrgcdartgretalnsvrlqslvlrrpcsrdsqslptpgafafht 180
 QY 181 EFHVPVGCCTCVLP RSV 197
 DB 181 efhvpvgctcvlprsv 197

RESULT 5
 ID AAY44460 standard; Protein: 197 AA.

AC AAY44460;
 DT 27-MAR-2000 (first entry)
 DE Human Interleukin 17C, PRO1122 polypeptide.
 XX Interleukin; IL-17C; PRO1122 polypeptide; clone DNA62377-1381-1; UNO561;
 KW cytokine IL-17; cytotoxic T-lymphocyte-associated antigen 8; CTR4-8;
 KM hybridisation probe; antagonist; degenerative cartilaginous disorder;
 XX agonist; diagnosis; therapy.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..18
 FT Protein /label- Signal_peptide
 FT 19..197
 FT /label- Mature_IL-17C-polypeptide
 FT /note- "Used to treat degenerative cartilaginous disorder"

FT Misc-difference 109 /note- "Conserved Trp residue"
 FT Misc-difference 129 /note- "Conserved Cys residue"
 FT Misc-difference 134 /note- "Conserved Cys residue"
 FT Misc-difference 163 /note- "Conserved Cys residue"
 FT Misc-difference 189 /note- "Conserved Cys residue"
 FT Misc-difference 191 /note- "Conserved Cys residue"
 XX W09960127-A2.
 XX 25-NOV-1999.
 XX 14-MAY-1999; 99WO-US10733.
 XX 15-MAY-1998; 98US-0085579.
 XX 23-DEC-1998; 98US-0113621.

(GENE) GENENTECH INC.

Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI;

DR WPI: 2000-116314/10.

DR N-PSDB: AAZ29728.

PT New polypeptides designated PRO1031 and PRO1122 used to treat a
 PT degenerative cartilaginous disorder

XX Claim 23; Fig 3; 141pp: English.

XX The present sequence is the human PRO1122 polypeptide, also referred to
 CC as UNO561, and as Interleukin-17C (IL-17C), encoded by
 CC clone DNA62377-1381-1. This sequence has identity with the
 CC cytokine IL-17 and cytotoxic T-lymphocyte-associated antigen 8 (CTLA-8)
 CC and has leucine zipper pattern. PRO1122 is expressed in pancreas, small
 CC intestine, stomach and testis also. It shares about 26-28% amino acid
 CC identity with IL-17 and IL-17B. The entire coding region of IL-17C can
 CC be used as hybridisation probe. The PRO1122 polypeptide, agonist or
 CC antagonist, is used to diagnose and treat a degenerative cartilaginous
 CC disorder.

XX Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 21; Length 197;
 Best Local Similarity 100.0%; Pred. No. 4.6e-109;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLFLTWLHTCLAHNDPSLRGPHSHGTPHCYSAEELPLGOAPPHLLARGAKWQ 60
 DB 1 mtlplglfltlwlnhtclahndpslrghshgtpchysaeelpigqaphllargakwq 60
 QY 61 ALPALVSSLEAASHRGHERPSATTOCPVLRPEEVLEADTHQHSISPMRYRVDTDEDRY 120
 DB 61 alpavlsleaashrgherpsattpcvlrpeeveleadthqrsispwryrvdtdedry 120
 QY 121 POKLAFAECCLRGCDARTGRETALNSVRLQSLVLRPRCSRDGSLPTPGAFAPFT 180
 DB 121 pklafaeclrgcdartgretalnsvrlqslvlrrpcsrdsqslptpgafafht 180
 QY 181 EFHVPVGCCTCVLP RSV 197
 DB 181 efhvpvgctcvlprsv 197

RESULT 6
 ID AAY53892 standard; Protein: 197 AA.

AC AAY53892;

DT 13-MAR-2000 (first entry)

DE Amino acid sequence of human Interleukin-21.

XX Human; Interleukin-22; IL-22; IL-21; Immune system disorder;
 KW Immune cell chemotaxis; haematopoietic cell disorder;
 KW haemostatic activity; thrombolytic activity; autoimmune disorder; asthma;
 KW respiratory problem; organ rejection; graft-versus-host disease; GVHD;
 KW inflammation; hyperproliferative disorder; tissue regeneration;
 KW embryonic stem cell differentiation; embryonic stem cell proliferation;
 KW haematopoietic lineage; allergic asthma.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..18 /note- "signal peptide"
 FT 34..40 /note- "conserved domain V"
 FT 63..68 /note- "conserved domain VI"
 FT 104..109 /note- "conserved domain VII"
 FT 113..121 /note- "conserved domain VII"

FT Domain

[illegible]